

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BROWNING, Jeffrey  
WARE, Carl
- (ii) TITLE OF INVENTION: LYMPHOTOKIN-BETA, LYMPHOTOKIN-BETA  
COMPLEXES, PHARMACEUTICAL PREPARATIONS AND THERAPEUTIC  
USES THEREOF
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: c/o FISH & NEAVE  
(B) STREET: 1251 Avenue of the Americas  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: U.S.A.  
(F) ZIP: 10020
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT/US91/04588  
(B) FILING DATE: 27-JUN-1991
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 07/544,862  
(B) FILING DATE: 27-JUN-1990
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: HALEY Jr., James F.  
(B) REGISTRATION NUMBER: 27,794  
(C) REFERENCE/DOCKET NUMBER: B129CIP11

TO/OF: T820400T

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 596-9000
- (B) TELEFAX: (212) 596-9090
- (C) TELEX: 14-8367

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CIG GGG CIG GAG GGC AGG GGT GGG AGG CTC CAG GGG AGG GGT TCC CTC	48
Leu Gly Leu Glu Gly Arg Gly Gly Arg Leu Gln Gly Arg Gly Ser Leu	
1 5 10 15	
CIG CTA GCT GIG GCA GGA GGC ACT TCT CIG GIG ACC TTG TTG CIG GCG	96
Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu Leu Leu Ala	
20 25 30	
GIG OCT ATC ACT GTC CIG GCT GIG CIG GGC TTA GIG CCC CAG GAT CAG	144
Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro Gln Asp Gln	
35 40 45	
GGA GGA CIG GTA ACG GAG ACG GGC GAC CCC GGG GCA CAG GGC CAG CAA	192
Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln Ala Gln Gln	
50 55 60	
GGA CIG GGG TTT CAG AAG CIG CCA GAG GAG GAG CCA GAA ACA GAT CTC	240
Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu Thr Asp Leu	
65 70 75 80	
AGC CCC GGG CTC CCA GCT GGC CAC CTC ATA GGC GCT CCG CIG AAG GGG	288
Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro Leu Lys Gly	
85 90 95	
CAG GGG CTA GGC TGG GAG ACG ACG AAG GAA CAG GCG TTT CIG ACG AGC	336
Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe Leu Thr Ser	
100 105 110	
GGG ACG CAG TTC TCG GAC GGC GAG GGG CIG GCG CTC CCG CAG GAC GGC	384
Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro Gln Asp Gly	
115 120 125	

10040221-10040221

CTC TAT TAC CTC TAC TGT CTC GTC GGC TAC CGG GGC GGC GGC OCT 432  
 Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg Ala Pro Pro  
 130 135 140

GGC GGC GGC GAC CCC CAG GGC CGC TGG GTC AGC CTG CGC AGC TCT CTG 480  
 Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg Ser Ser Leu  
 145 150 155 160

TAC CGG GGC GGC GGC GGC TAC GGC CGC GGC ACT CCC GAG CTG CTG CTC 528  
 Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu Leu Leu Leu  
 165 170 175

GAG GGC GGC GAG AGC GTG ACT CCA GTG CTG GAC CGC GGC AGG AGA CAA 576  
 Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala Arg Arg Gln  
 180 185 190

GGG TAC GGC OCT CTC TGG TAC AGC AGC GTG GGC TTC GGC GGC CTG GTG 624  
 Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly Gly Leu Val  
 195 200 205

CAG CTC CGG AGG GGC GAG AGG GTG TAC GTC AAC ATC AGT CAC CCC GAT 672  
 Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile Ser His Pro Asp  
 210 215 220

ATG GTG GAC TTC GGC AGA GGC AAG ACC TTC TTT GGC GGC GTG ATG GTG 720  
 Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly Ala Val Met Val  
 225 230 235 240

GGG TGA 726  
 Gly

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Gly Leu Glu Gly Arg Gly Gly Arg Leu Gln Gly Arg Gly Ser Leu  
 1 5 10 15

Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu Leu Ala  
 20 25 30

Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro Gln Asp Gln  
 35 40 45

Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln Ala Gln Gln  
 50 55 60

Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu Thr Asp Leu  
65 70 75 80

Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro Leu Lys Gly  
85 90 95

Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe Leu Thr Ser  
100 105 110

Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro Gln Asp Gly  
115 120 125

Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg Ala Pro Pro  
130 135 140

Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg Ser Ser Leu  
145 150 155 160

Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu Leu Leu Leu  
165 170 175

Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala Arg Arg Gln  
180 185 190

Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly Gly Leu Val  
195 200 205

Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile Ser His Pro Asp  
210 215 220

Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly Ala Val Met Val  
225 230 235 240

Gly

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTG GCC TTA GTG CCC CAG GAT CAG GGA GGA CTG GTA ACG GAG ACG GGC  
Leu Ala Leu Val Pro Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala  
1 5 10 15

GAC CCG GGG GCA CAG GCC CAG CAA GGA CTG GGG TTT CAG AAG CTG CCA Asp Pro Gly Ala Gln Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro 20 25 30	96
GAG GAG GAG CCA GAA ACA GAT CTC AGC CCG GGG CTC CCA GCT GCC CAC Glu Glu Glu Pro Glu Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His 35 40 45	144
CTC ATA GGC GCT CCG CTG AAG GGG CAG GGG CTA GGC TGG GAG ACG ACG Leu Ile Gly Ala Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr 50 55 60	192
AAG GAA CAG GCG TTT CTG ACG AGC GGG ACG CAG TTC TCG GAC GCC GAG Lys Glu Gln Ala Phe Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu 65 70 75 80	240
GGG CTG GCG CTC CCG CAG GAC GGC CTC TAT TAC CTC TAC TGT CTC GTC Gly Leu Ala Leu Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val 85 90 95	288
GGC TAC CCG GGC CCG GCG CCG CCG GGC GGC GGC GAC CCG CAG GGC CCG Gly Tyr Arg Gly Arg Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg 100 105 110	336
TCG GTC ACG CTG CCG AGC TCT CTG TAC CCG GCG GGC GGC GGC TAC GGC Ser Val Thr Leu Arg Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly 115 120 125	384
CCG GGC ACT CCG GAG CTG CTG CTC GAG GGC GGC GAG ACG GTC ACT CCA Pro Gly Thr Pro Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro 130 135 140	432
GTC CTG GAC CCG GCC AGG AGA CAA GGG TAC GGG OCT CTC TGG TAC ACG Val Leu Asp Pro Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr 145 150 155 160	480
AGC GTC GGG TTC GGC GGC CTG GTC CAG CTC CCG AGG GGC GAG AGG GTC Ser Val Gly Phe Gly Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val 165 170 175	528
TAC GTC AAC ATC AGT CAC CCG GAT ATG GTC GAC TTC GCG AGA GGG AAG Tyr Val Asn Ile Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys 180 185 190	576
AAC TTC TTT GGG GCC GTC ATG GTC GGG TGA Thr Phe Phe Gly Ala Val Met Val Gly 195 200	606

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

102011-13204001

(ii) MOLECULE TYPE: protein

(xci) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Leu Ala Leu Val Pro Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala
 1             5             10             15
Asp Pro Gly Ala Gln Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro
      20             25             30
Glu Glu Glu Pro Glu Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His
      35             40             45
Leu Ile Gly Ala Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr
      50             55             60
Lys Glu Gln Ala Phe Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu
      65             70             75             80
Gly Leu Ala Leu Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val
      85             90             95
Gly Tyr Arg Gly Arg Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg
      100            105            110
Ser Val Thr Leu Arg Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly
      115            120            125
Pro Gly Thr Pro Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro
      130            135            140
Val Leu Asp Pro Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr
      145            150            155            160
Ser Val Gly Phe Gly Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val
      165            170            175
Tyr Val Asn Ile Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys
      180            185            190
Thr Phe Phe Gly Ala Val Met Val Gly
      195            200

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCG CIG AAG GGG CAG GGG CTA GGC TGG GAG ACG ACG AAG GAA CAG GCG	48
Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala	
1 5 10 15	
TTT CIG ACG AGC GGG AGC CAG TTC TCG GAC GGC GAG GGG CIG GCG CTC	96
Phe Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu	
20 25 30	
CCG CAG GAC GGC CTC TAT TAC CTC TAC TGT CTC GTC GGC TAC CCG GCG	144
Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly	
35 40 45	
CGG GCG CCC CCT GGC GGC GGG GAC CCC CAG GGC CGC TCG GTC ACG CIG	192
Arg Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu	
50 55 60	
CGC AGC TCT CIG TAC CGG GCG GGG GGC GGC TAC GGG CGG GGC ACT CCC	240
Arg Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro	
65 70 75 80	
GAG CIG CIG CTC GAG GGC GGC GAG ACG GIG ACT CCA GIG CIG GAC CCG	288
Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro	
85 90 95	
GCC AGG AGA CAA GGG TAC GGG CCT CTC TGG TAC ACG AGC GIG GGG TTC	336
Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe	
100 105 110	
GGC GGC CIG GIG CAG CTC CGG AGG GGC GAG AGG GIG TAC GTC AAC ATC	384
Gly Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile	
115 120 125	
AGT CAC CCC GAT ATG GIG GAC TTC GCG AGA GGG AAG ACC TTC TTT GGG	432
Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly	
130 135 140	
GCC GIG ATG GIG GGG TGA	450
Ala Val Met Val Gly	
145	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

10040231.1090

Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala  
 1 5 10 15  
 Phe Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu  
 20 25 30  
 Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly  
 35 40 45  
 Arg Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu  
 50 55 60  
 Arg Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro  
 65 70 75 80  
 Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro  
 85 90 95  
 Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe  
 100 105 110  
 Gly Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile  
 115 120 125  
 Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly  
 130 135 140  
 Ala Val Met Val Gly  
 145

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CIG GGC TTA GIG CCC CAG GAT CAG GGA GGA CIG GTA ACG GAG ACG GGC	48
Leu Ala Leu Val Pro Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala	
1 5 10 15	
GAC CCC GGG GCA CAG GGC CAG CAA GGA CIG GGG TTT CAG AAG CIG CCA	96
Asp Pro Gly Ala Gln Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro	
20 25 30	

10040331-1000



GAG GAG GAG CCA GAA ACA GAT CTC AGC CCC GGG CTC CCA GCT GCC CAC 144  
 Glu Glu Glu Pro Glu Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His  
                   35                  40                  45

CTC ATA GGC GCT 156  
 Leu Ile Gly Ala  
                   50

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Ala Leu Val Pro Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala  
   1                  5                  10                  15  
 Asp Pro Gly Ala Gln Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro  
                   20                  25                  30  
 Glu Glu Glu Pro Glu Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His  
                   35                  40                  45  
 Leu Ile Gly Ala  
                   50

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHEetical: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTATTGGCT CTCTCTC

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GYTONGGTT CYTCATC

17

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGGGGCAC TGGGGCTG

18

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10040931.10701  
T02011 T3204001

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /function= "linker"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "The 5' terminal 4 nucleotides in the complementary strand are not present in this linker "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCGGCGCCTT TAGAGCACA

19

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACAGTGATA GGCAAGGACA GCAACAA

27

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T02011" T8204001